

In the Specification

Please substitute the Brief Description Of The Drawings at pages 48-50, with the following  
Brief Description Of The Drawings:

**Brief Description Of The Drawings**

- Figure 1.** Schematic representation of the PKC isozymes domain structure
- Figure 2.** A schematic representation of PKC $\beta$  sequence as deduced from the cDNA analysis
- Figure 3.** Alternative splicing of PKC $\beta$  pre-mRNA
- Figure 4.** PKC $\beta$ II mRNA is generated via exon inclusion in the alternative splicing of PKC $\beta$
- Figure 5.** Generation of PKC activators
- Figure 6.** Activation of PKC by diacylglycerol and Ca $+2$
- Figure 7.** Model for activation of PKC
- Figure 8.** Localization of PKC isozymes by anchoring proteins
- Figure 9.** Arterial smooth muscle cell phenotypes
- Figure 10.** Representation of the response-to-injury hypothesis of atherosclerosis proposed by Ross
- Figure 11.** The MAP kinase pathway transduces the signal from the membrane to the nucleus
- Figure 12.** The role of phosphoinositide 3-kinase (PI3 kinase) in signal transduction
- Figure 13.** Levels of eukaryotic gene regulation
- Figure 14.** The fate of mRNA in mammalian cells
- Figure 15.** Representation of the structural elements involved in regulating mRNA stability
- Figure 16.** PKC $\beta$ I protein levels remain unaltered in the presence of high glucose
- Figure 17.** PKC $\beta$ II protein levels decreased by 55% in the presence of glucose
- Figure 18.** Down regulation of PKC $\beta$ (I+II) mRNA by glucose
- Figure 19.** Map of PKC $\beta$  promoter and lengths of deletion constructs
- Figure 20.** Effect of high glucose on PKC $\beta$  deletion constructs
- Figure 21.** Construct D quenches PKC $\beta$  promoter activity at 10h post-synchronization corresponding to S phase
- Figure 22.** Northern blot analysis of PKC $\beta$ II mRNA in A10 cells treated with actinomycin D in the presence or absence of high glucose

**Figure 23.** *In vitro* assay for RNA stability

**Figure 24.** *In vitro* assay for RNA stability in the presence of EDTA

**Figure 25.** A schematic representation of the PKC $\beta$  as deduced from cDNA sequence analysis

**Figure 26.** High glucose destabilizes PKC $\beta$ II mRNA

**Figure 27.** PKC  $\beta$ II cDNA (350 bp) sequence (SEQ ID NO: 8)

**Figure 28.** PKC  $\beta$ II cDNA (350 bp) restriction sites map

**Figure 29.** Effect of glucose and insulin on PKC $\beta$ II mRNA in aorta smooth muscle cells

**Figure 30.** Glucosamine does not affect PKC $\beta$ II mRNA stability

**Figure 31.** Effect of glucose metabolites on PKC $\beta$ II mRNA stability

**Figure 32.** Effect of cycloheximide on glucose-induced PKC $\beta$ II destabilization

**Figure 33.** RT-PCR analysis of PKC $\beta$ I and  $\beta$ II mRNA after okadaic acid treatment

**Figure 34.** The p $\beta$ G-PKC $\beta$ II chimeric minigene

**Figure 35.** The p $\beta$ G-PKC $\beta$ II chimeric minigene is destabilized by high glucose

**Figure 36.** Half-life analysis of p $\beta$ G-PKC $\beta$ II mRNA

**Figure 37.** Schematic of the RNA probes used for the RNA EMSAs

**Figure 38.** RNA electrophoretic mobility shift assay using full length PKC $\beta$ II mRNA probe

**Figure 39.** A cytosolic factor binds to a glucose-regulated element present in the PKC $\beta$ II coding region

**Figure 40.** No RNA protein binding observed using RNA probe C

**Figure 41.** UV cross-linking analysis of the RNA-protein binding complex

**Figure 42.** PKC $\beta$ II mRNA sequence (SEQ ID NO: 10) and RNA secondary structure analysis

**Figure 43.** PKC $\beta$ II mRNA sequence linearized at 175 bp with *Bgl* II (SEQ ID NO: 11) and RNA secondary structure analysis

**Figure 44.** PKC $\beta$ II mRNA sequence linearized at 137 bp with *Hpa* I (SEQ ID NO: 12) and RNA secondary structure analysis

**Figure 45.** Diagram of 3' exons encoding PKC $\beta$ I and PKC $\beta$ II via exon inclusion/exclusion and regions of PKC $\beta$ II exon involved in destabilization of mRNA.

**Figure 46.** Restriction map of 3' region of PKC $\beta$ II exon with portions of 3' and 5' flanking exons to be cloned downstream of the cDNA of interest.

Please insert the following Brief Description of the Sequences at page 51, line 1, before the Detailed Description of the specification and after the Brief Description of the Drawings:

Brief Description of the Sequences

SEQ ID NO: 1 is the amino acid sequence of tyrosine phosphatase conserved active-site motif.

SEQ ID NO: 2 is the amino acid sequence of tyrosine phosphatase signature sequence motif.

SEQ ID NO: 3 is the amino acid sequence of dual-specificity phosphatase signature sequence motif.

SEQ ID NO: 4 is the nucleotide sequence of PKC $\beta$ I and PKC $\beta$ II upstream sense primer.

SEQ ID NO: 5 is the nucleotide sequence of PKC $\beta$ I downstream anti-sense primer.

SEQ ID NO: 6 is the nucleotide sequence of  $\beta$ -globin sense primer.

SEQ ID NO: 7 is the nucleotide sequence of  $\beta$ -globin anti-sense primer.

SEQ ID NO: 8 is the nucleotide sequence of 350 basepairs of PKC $\beta$ II cDNA.

SEQ ID NO: 9 is the nucleotide sequence of the metabolite responsive instability element within PKC $\beta$ II cDNA.

SEQ ID NO: 10 is the nucleotide sequence of PKC $\beta$ II mRNA.

SEQ ID NO: 11 is the partial nucleotide sequence of PKC $\beta$ II mRNA.

SEQ ID NO: 12 is the partial nucleotide sequence of PKC $\beta$ III mRNA.

SEQ ID NO: 13 is the amino acid sequence of protein kinase ATP-binding motif.

Please delete existing pages 1-5 of the Sequence Listing and insert the attached new pages 1-5 of the Sequence Listing at the end of the specification.